

SEQUENCE LISTING

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<110> ALBANI, SALVATORE
 <120> METHOD FOR ISOLATION, QUANTIFICATION, CHARACTERIZATION
       AND MODULATION OF ANTIGEN-SPECIFIC T CELLS
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 <140> 10/617,639
 <141> 2003-07-07
 <150> 09/756,983
<151> 2001-01-09
<150> PCT/US99/24666
<151> 1999-10-19
<150> 09/421,506
<151> 1999-10-19
<150> 60/105,018
<151> 1998-10-20
<160> 24
<170> PatentIn Ver. 2.1
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<223> Description of Artificial Sequence: Synthetic peptide derived
      from third hyper V region of IE molecule of Mus musculus
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      from bole I protein of Epstein Barr virus
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Thr Arg Asp Asp Ala Glu Tyr Leu Leu Gly Arg Glu Ser Val Leu
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<223> Description of Artificial Sequence: Synthetic peptide derived
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Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
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      from the TCR receptor of Mus musculus
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<221> MOD_RES
<222> (18)
<223> Ser, Ile or Thr
Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys
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Ala Xaa Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro
Gly Thr Arg Leu
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<213> Artificial Sequence
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<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic peptide derived
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<223> Description of Artificial Sequence: Synthetic peptide derived
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<223> Description of Artificial Sequence: Synthetic peptide
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Arg
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cct gaa act Pro Glu Thr 195	gag ctc Glu Leu	tat gct Tyr Ala	gtt a Val S 200	igc gaa Ser Glu	ttc ggc Phe Gly	ggc Gly 205	tcc Ser	ggt Gly	ggt Gly	624
agc gcc aca Ser Ala Thr 210	cct caa Pro Gln	aat att Asn Ile 215	act g Thr A	gat ttg Asp Leu	tgt gca Cys Ala 220	gaa Glu	tac Tyr	cac His	aac Asn	672
aca caa ata Thr Gln Ile 225	cat acg His Thr	cta aat Leu Asn 230	gat a Asp L	aag ata Lys Ile	ttt tcg Phe Ser 235	tat Tyr	aca Thr	gaa Glu	tct Ser 240	720
cta gct gga Leu Ala Gly	aaa aga Lys Arg 245	gag atg Glu Met	gct a Ala I	atc att [le Ile 250	act ttt Thr Phe	aag Lys	aat Asn	ggt Gly 255	gca Ala	768
act ttt caa Thr Phe Gln	gta gaa Val Glu 260	gta cca Val Pro	Gly S	agt caa Ser Gln 265	cat ata His Ile	gat Asp	tca Ser 270	caa Gln	aaa Lys	816
aaa gcg att Lys Ala Ile 275	gaa agg Glu Arg	atg aag Met Lys	gat a Asp T 280	acc ctg Thr Leu	agg att Arg Ile	gca Ala 285	tat Tyr	ctt Leu	act Thr	864
gaa gct aaa Glu Ala Lys 290	gtc gaa Val Glu	aag tta Lys Leu 295	tgt g Cys V	gta tgg Val Trp	aat aat Asn Asn 300	Lys	acg Thr	cct Pro	cat His	912
gcg att gcc Ala Ile Ala 305										942
<210> 16 <211> 313 <212> PRT <213> Artif	icial Sed	quence								
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Leu Asn Phe	Phe Gln 20	Leu Leu	Val I	Leu Ala 25	Gly Leu	Ser	His 30	Phe	Cys	
Ser Gly Val	Ile His	Val Thr	Lys G	Glu Val	Lys Glu	Val 45	Ala	Thr	Leu	
Ser Cys Gly 50	His Asn	Val Ser 55		Glu Glu	Leu Ala		Thr	Arg	Ile	

Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
70 75 80

Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr

Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly

Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg 115 120 125

Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr 130 140

Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile 145 150 155 160

Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu 165 170 175

Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp 180 185 190

Pro Glu Thr Glu Leu Tyr Ala Val Ser Glu Phe Gly Gly Ser Gly Gly 195 200 205

Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu Tyr His Asn 210 215 220

Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr Thr Glu Ser 225 230 235 240

Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala 245 250 255

Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys 260 265 270

Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala Tyr Leu Thr 275 280 285

Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys Thr Pro His 290 295 300

Ala Ile Ala Ala Ile Ser Met Ala Asn 305 310

<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion construct with

human and bacterial sequences

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gct Ala	gct Ala	cct Pro	ctg Leu 20	aag Lys	att Ile	caa Gln	gct Ala	tat Tyr 25	ttc Phe	aat Asn	gag Glu	act Thr	gca Ala 30	gac Asp	ctg Leu	96
cca Pro	tgc Cys	caa Gln 35	ttt Phe	gca Ala	aac Asn	tct Ser	caa Gln 40	aac Asn	caa Gln	agc Ser	ctg Leu	agt Ser 45	gag Glu	cta Leu	gta Val	144
gta Val	ttt Phe 50	tgg Trp	cag Gln	gac Asp	cag Gln	gaa Glu 55	aac Asn	ttg Leu	gtt Val	ctg Leu	aat Asn 60	gag Glu	gta Val	tac Tyr	tta Leu	192
ggc Gly 65	aaa Lys	gag Glu	aaa Lys	ttt Phe	gac Asp 70	agt Ser	gtt Val	cat His	tcc Ser	aag Lys 75	tat Tyr	atg Met	ggc Gly	cgc Arg	aca Thr 80	240
agt Ser	ttt Phe	gat Asp	tcg Ser	gac Asp 85	agt Ser	tgg Trp	acc Thr	ctg Leu	aga Arg 90	ctt Leu	cac His	aat Asn	ctt Leu	cag Gln 95	atc Ile	288
aag Lys	gac Asp	aag Lys	ggc Gly 100	ttg Leu	tat Tyr	caa Gln	tgt Cys	atc Ile 105	atc Ile	cat His	cac His	aaa Lys	aag Lys 110	ccc Pro	aca Thr	336
gga Gly	atg Met	att Ile 115	cgc Arg	atc Ile	cac His	cag Gln	atg Met 120	aat Asn	tct Ser	gaa Glu	ctg Leu	tca Ser 125	gtg Val	ctt Leu	gct Ala	384
aac Asn	ttc Phe 130	agt Ser	caa Gln	cct Pro	gaa Glu	ata Ile 135	gta Val	cca Pro	att Ile	tct Ser	aat Asn 140	ata Ile	aca Thr	gaa Glu	aat Asn	432
gtg Val 145	tac Tyr	ata Ile	aat Asn	ttg Leu	acc Thr 150	tgc Cys	tca Ser	tct Ser	ata Ile	cac His 155	ggt Gly	tac Tyr	cca Pro	gaa Glu	cct Pro 160	480
aag Lys	aag Lys	atg Met	agt Ser	gtt Val 165	ttg Leu	cta Leu	aga Arg	acc Thr	aag Lys 170	aat Asn	tca Ser	act Thr	atc Ile	gag Glu 175	tat Tyr	528
gat Asp	ggt Gly	att Ile	atg Met 180	cag Gln	aaa Lys	tct Ser	caa Gln	gat Asp 185	aat Asn	gtc Val	aca Thr	gaa Glu	ctg Leu 190	Tyr	gac Asp	576

gtt Val	tcc Ser	atc Ile 195	agc Ser	ttg Leu	tct Ser	gtt Val	tca Ser 200	ttc Phe	cct Pro	gat Asp	gtt Val	acg Thr 205	agc Ser	aat Asn	atg Met	624
acc Thr	atc Ile 210	ttc Phe	tgt Cys	att Ile	ctg Leu	gaa Glu 215	act Thr	gac Asp	aag Lys	acg Thr	cgg Arg 220	ctt Leu	tta Leu	tct Ser	tca Ser	672
cct Pro 225	ttc Phe	tct Ser	ata Ile	gag Glu	ctt Leu 230	gag Glu	gac Asp	cct Pro	cag Gln	cct Pro 235	ccc Pro	cca Pro	gac Asp	cac His	gaa Glu 240	720
ttc Phe	ggc Gly	ggc Gly	tcc Ser	ggt Gly 245	ggt Gly	agc Ser	gcc Ala	aca Thr	cct Pro 250	caa Gln	aat Asn	att Ile	act Thr	gat Asp 255	ttg Leu	768
tgt Cys	gca Ala	gaa Glu	tac Tyr 260	cac His	aac Asn	aca Thr	caa Gln	ata Ile 265	cat His	acg Thr	cta Leu	aat Asn	gat Asp 270	aag Lys	ata Ile	816
ttt Phe	tcg Ser	tat Tyr 275	aca Thr	gaa Glu	tct Ser	cta Leu	gct Ala 280	gga Gly	aaa Lys	aga Arg	gag Glu	atg Met 285	gct Ala	atc Ile	att Ile	864
act Thr	ttt Phe 290	aag Lys	aat Asn	ggt Gly	gca Ala	act Thr 295	ttt Phe	caa Gln	gta Val	gaa Glu	gta Val 300	cca Pro	ggt Gly	agt Ser	caa Gln	912
cat His 305	ata Ile	gat Asp	tca Ser	caa Gln	aaa Lys 310	aaa Lys	gcg Ala	att Ile	gaa Glu	agg Arg 315	atg Met	aag Lys	gat Asp	acc Thr	ctg Leu 320	960
						gaa Glu										1008
aat Asn	aat Asn	aaa Lys	acg Thr 340	cct Pro	cat His	gcg Ala	att Ile	gcc Ala 345	gca Ala	att Ile	agt Ser	atg Met	gca Ala 350	aat Asn	taa	1056

<210> 18

<211> 351 <212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Fusion construct with human and bacterial sequences

<400> 18

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- Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu 50 55 60
- Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
 65 70 75 80
- Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile 85 90 95
- Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr 100 105 110
- Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala 115 120 125
- Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn 130 135 140
- Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro 145 150 155 160
- Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
- Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp 180 185 190
- Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met 195 200 205
- Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser 210 215 220
- Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu 225 230 235 240
- Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu 245 250 255
- Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile 260 265 270
- Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile 275 280 285
- Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln 290 295 300
- His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu 305 310 315 320
- Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp 325 330 335

Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn

340

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<213> Artificial Sequence
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Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
                                 25
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<211> 30
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic peptide
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Leu Lys Gln Lys Leu Gln Ala Leu Lys Lys Lys Leu Ala Gln
<210> 21
<211> 1095
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<213> Artificial Sequence
<223> Description of Artificial Sequence: Fusion construct with
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<222> (1)..(1092)
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Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
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atc Ile	cag Gln	gcc Ala 35	gag Glu	ttc Phe	tat Tyr	ctg Leu	aat Asn 40	cct Pro	gac Asp	caa Gln	tca Ser	ggc Gly 45	gag Glu	ttt Phe	atg Met	144
ttt Phe	gac Asp 50	ttt Phe	gat Asp	ggt Gly	gat Asp	gag Glu 55	att Ile	ttc Phe	cat His	gtg Val	gat Asp 60	atg Met	gca Ala	aag Lys	aag Lys	192
gag Glu 65	acg Thr	gtc Val	tgg Trp	cgg Arg	ctt Leu 70	gaa Glu	gaa Glu	ttt Phe	gga Gly	cga Arg 75	ttt Phe	gcc Ala	agc Ser	ttt Phe	gag Glu 80	240
gct Ala	caa Gln	ggt Gly	gca Ala	ttg Leu 85	gcc Ala	aac Asn	ata Ile	gct Ala	gtg Val 90	gac Asp	aaa Lys	gcc Ala	aac Asn	ctg Leu 95	gaa Glu	288
atc Ile	atg Met	aca Thr	aag Lys 100	cgc Arg	tcc Ser	aac Asn	tat Tyr	act Thr 105	ccg Pro	atc Ile	acc Thr	aat Asn	gta Val 110	cct Pro	cca Pro	336
gag Glu	gta Val	act Thr 115	gtg Val	ctc Leu	acg Thr	aac Asn	agc Ser 120	cct Pro	gtg Val	gaa Glu	ctg Leu	aga Arg 125	gag Glu	ccc Pro	aac Asn	384
gtc Val	ctc Leu 130	atc Ile	tgt Cys	ttc Phe	atc Ile	gac Asp 135	aag Lys	ttc Phe	acc Thr	cca Pro	cca Pro 140	gtg Val	gtc Val	aat Asn	gtc Val	432
acg Thr 145	tgg Trp	ctt Leu	cga Arg	aat Asn	gga Gly 150	aaa Lys	cct Pro	gtc Val	acc Thr	aca Thr 155	gga Gly	gtg Val	tca Ser	gag Glu	aca Thr 160	480
gtc Val	ttc Phe	ctg Leu	ccc Pro	agg Arg 165	gaa Glu	gac Asp	cac His	ctt Leu	ttc Phe 170	cgc Arg	aag Lys	ttc Phe	cac His	tat Tyr 175	ctc Leu	528
													gtg Val 190			576
tgg Trp	ggc	ttg Leu 195	gat Asp	gag Glu	cct Pro	ctt Leu	ctc Leu 200	aag Lys	cac His	tgg Trp	gag Glu	ttt Phe 205	gat Asp	gct Ala	cca Pro	624
agc Ser	cct Pro 210	Leu	cca Pro	gag Glu	act Thr	aca Thr 215	gag Glu	gaa Glu	ttc Phe	ggt Gly	ggt Gly 220	Ser	ggt Gly	ggt Gly	tcc Ser	672
gcg Ala 225	Gln	ctg Leu	gaa Glu	tgg Trp	gaa Glu 230	ctg Leu	cag Gln	gcg Ala	ctg Leu	gaa Glu 235	Lys	gaa Glu	aac Asn	gcg Ala	cag Gln 240	720

ctg Leu	gaa Glu	tgg Trp	gaa Glu	ctg Leu 245	cag Gln	gcg Ala	ctg Leu	gaa Glu	aaa Lys 250	gaa Glu	ctg Leu	gcg Ala	cag Gln	ggc Gly 255	ggc Gly	768
tcc Ser	ggt Gly	ggt Gly	agc Ser 260	gcc Ala	aca Thr	cct Pro	caa Gln	aat Asn 265	att Ile	act Thr	gat Asp	ttg Leu	tgt Cys 270	gca Ala	gaa Glu	816
tac Tyr	cac His	aac Asn 275	aca Thr	caa Gln	ata Ile	cat His	acg Thr 280	cta Leu	aat Asn	gat Asp	aag Lys	ata Ile 285	ttt Phe	tcg Ser	tat Tyr	864
aca Thr	gaa Glu 290	tct Ser	cta Leu	gct Ala	gga Gly	aaa Lys 295	aga Arg	gag Glu	atg Met	gct Ala	atc Ile 300	att Ile	act Thr	ttt Phe	aag Lys	912
aat Asn 305	ggt Gly	gca Ala	act Thr	ttt Phe	caa Gln 310	gta Val	gaa Glu	gta Val	cca Pro	ggt Gly 315	agt Ser	caa Gln	cat His	ata Ile	gat Asp 320	960
tca Ser	caa Gln	aaa Lys	aaa Lys	gcg Ala 325	att Ile	gaa Glu	agg Arg	atg Met	aag Lys 330	gat Asp	acc Thr	ctg Leu	agg Arg	att Ile 335	gca Ala	1008
tat Tyr	ctt Leu	act Thr	gaa Glu 340	gct Ala	aaa Lys	gtc Val	gaa Glu	aag Lys 345	tta Leu	tgt Cys	gta Val	tgg Trp	aat Asn 350	aat Asn	aaa Lys	1056
acg Thr	cct Pro	cat His 355	gcg Ala	att Ile	gcc Ala	gca Ala	att Ile 360	agt Ser	atg Met	gca Ala	aat Asn	taa				1095
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Leu	Met	Ser	Ala 20		Glu	Ser	Trp	Ala 25	Ile	Lys	Glu	Glu	His 30		Ile	
Ile	Gln	Ala 35		Phe	Tyr	Leu	Asn 40		Asp	Gln	Ser	Gly 45		Phe	Met	
Phe	Asp 50	Phe	Asp	Gly	Asp	Glu 55		Phe	His	Val	Asp 60		Ala	Lys	Lys	
Glu 65	Thr	Val	Trp	Arg	Leu 70		Glu	Phe	Gly	Arg 75		Ala	Ser	Phe	Glu 80	

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn 120 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val . 130 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr 155 150 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu 170 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His 185 180 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln 235 230 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu 265 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr 280 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala 325 330 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys

Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn 355 360

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	Gln													gaa Glu		576
_	cct Pro		_			_			_						_	624
_	acg Thr 210	_					_		_	_			_		_	672
	agc Ser															720
	gct Ala															768
ctg Leu	aag Lys	aaa Lys	aag Lys 260	ctg Leu	gct Ala	cag Gln	ggt Gly	tcc Ser 265	ggt Gly	ggt Gly	tcc Ser	gcg Ala	gġt Gly 270	ggt Gly	ggt Gly	816
	aac Asn												ţaat	aa		861
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- Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr 100 105 110
- Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
- Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu 130 135 140
- Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp 145 150 155 160
- Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu 165 170 175
- Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr 180 185 190
- Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser 195 200 205
- Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala 210 215 220
- Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Leu 225 230 235
- Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala 245 250 255
- Leu Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly 260 265 270
- Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His 275 280 280